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Draft Genome Sequence of *Staphylococcus cohnii* subsp. *urealyticus* Isolated from a Healthy Dog

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ABSTRACT *Staphylococcus cohnii* subsp. *urealyticus* strain SW120 was isolated from the ear swab of a healthy dog. The isolate is resistant to methicillin and fusidic acid. The SW120 draft genome is 2,805,064 bp and contains 2,667 coding sequences, including 58 tRNAs and nine complete rRNA coding regions.

As part of our effort to elucidate antibiotic resistance mechanisms among *Staphylococci* species recovered from companion animals, *S. cohnii* subsp. *urealyticus* strain SW120 was isolated from an ear swab of a 2-year-old female Weimaraner living in Ballarat, Australia. *S. cohnii* subsp. *urealyticus* was first described in 1991 (1) and methicillin-resistant strains have been recovered previously from companion animals (2, 3).

The isolate was recovered after enriching an ear swab in tryptic soya broth supplemented with 8% NaCl and incubated at 37°C for 24 h before subculture to Baird-Parker agar at 37°C for 48 h. The isolate was coagulase-negative in rabbit plasma, DNase-negative, and novobiocin-resistant. Sequencing of the 16SrRNA gene was unable to conclusively identify the isolate: this is consistent with previous reports that 16SrRNA sequencing has limited discriminatory ability among *Staphylococci* species (4). Instead, sequencing of housekeeping genes, including *cpn60* (5), *dnaJ* (4), *rpoB* (6, 7), and *tuf* (8) are preferred for speciation and in each case identified the isolate as *S. cohnii* subsp. *urealyticus* at ≥98% sequence identity. This was further confirmed by biochemical testing, in particular, the prolific hydrolysis of urea.

Sequencing was performed on the Illumina MiSeq platform (Illumina, Inc., San Diego, CA, USA). The closest available reference genome was identified using Kraken, and the reads were mapped to this using the Burrows–Wheeler aligner “mem” (BWA-mem) algorithm version 2 to assess the quality of the data. A *de novo* assembly of the reads was performed using SPAdes version 3.7.1, and the reads were again mapped back to the resultant contigs using BWA-mem. The assembly comprised 24 contigs (>1,000 bp) with a total length of 2,805,064 bp and a G+C content of 32.43% and an N_{50} value of 661,385 bp. Annotation was performed by the NCBI Prokaryote Genome Annotation Pipeline (PGAP) which showed a total of 2,667 coding sequences, including at least 58 tRNAs, nine complete rRNAs, and two CRISPR arrays.

ResFinder version 2.1 (9) failed to find any resistance determinants despite the isolate being phenotypically resistant to methicillin (by oxacillin and cefoxitin disk diffusion) and fusidic acid (MIC 4 μg/mL). Subsequent analysis of the genome identified a putative 238-residue protein with 100% identity to a putative *mecA* gene from an *S. cohnii* subsp. *cohnii* isolate. Fusidic acid resistance was imparted by the recently described *fusF* gene (10).

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Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [MPPU0000000](https://doi.org/10.1093/jac/dkt020). The version described in this paper is the first version, MPPU01000000.

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